



2/20

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/002,309A  
Source: CIPE  
Date Processed by STIC: 2/26/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

01PE

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/002,309A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220>  
Sequence(s) 2 missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply  
Corrected Diskette Needed

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/002,309A

DATE: 02/26/2002

TIME: 14:53:40

Input Set : A:\B0122173.txt

Output Set: N:\CRF3\02262002\J002309A.raw

Error on P. 6

3 <110> APPLICANT: Welch, Rodney A.  
 4 Lathem, Wyndham W.  
 6 <120> TITLE OF INVENTION: E. COLI O157:H7 C1 ESTERASE INHIBITOR-BINDING PROTEIN AND  
 METHODS OF USE  
 8 <130> FILE REFERENCE: 096429-9117  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/002,309A  
 11 <141> CURRENT FILING DATE: 2001-10-26  
 13 <150> PRIOR APPLICATION NUMBER: 60/243,675  
 14 <151> PRIOR FILING DATE: 2000-10-26  
 16 <160> NUMBER OF SEQ ID NOS: 17  
 18 <170> SOFTWARE: PatentIn version 3.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 2798  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Unknown Organism  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (138)..(2798)  
 28 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid  
 p0157  
 31 <400> SEQUENCE: 1  
 32 tttagcgaac aggtgtaaat atgttataaa aataaccaac gactagtga taagtcgctc 60  
 34 ctgaaaaaat aaaatataga aataactgtta tatccggctg catgaacact aaaatgaatg 120  
 36 agagatggag aacaccg atg aaa tta aag tat ctg tca tgt acg atc ctt 170  
 37 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu  
 38 1 5 10  
 40 gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat 218  
 41 Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn  
 42 15 20 25  
 44 tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt 266  
 45 Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly  
 46 30 35 40  
 48 tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc 314  
 49 Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala  
 50 45 50 55  
 52 cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa 362  
 53 His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys  
 54 60 65 70 75  
 56 agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt 410  
 57 Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val  
 58 80 85 90  
 60 cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc 458  
 61 Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr  
 62 95 100 105

64 ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt

506

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Input Set : A:\B0122173.txt

Output Set: N:\CRF3\02262002\J002309A.raw

65	Leu	Tyr	Pro	Pro	Ser	Ser	Leu	Pro	Asp	Thr	Ile	Tyr	His	Leu	Asp	Gly	
66			110					115					120				
68	gtt	ccg	gaa	ggt	ggt	atc	gat	ttc	aca	cct	cat	aat	gga	acg	aaa	aag	554
69	Val	Pro	Glu	Gly	Gly	Ile	Asp	Phe	Thr	Pro	His	Asn	Gly	Thr	Lys	Lys	
70		125					130					135					
72	atc	att	aat	acg	gtg	gct	gaa	gta	aac	aaa	ctc	agt	gat	gcc	agc	ggg	602
73	Ile	Ile	Asn	Thr	Val	Ala	Glu	Val	Asn	Lys	Leu	Ser	Asp	Ala	Ser	Gly	
74	140					145					150					155	
76	agt	tct	att	cat	agc	cat	cta	aca	aat	aat	gca	ctg	gtg	gag	atc	cat	650
77	Ser	Ser	Ile	His	Ser	His	Leu	Thr	Asn	Asn	Ala	Leu	Val	Glu	Ile	His	
78				160						165					170		
80	act	gca	aat	ggt	cgt	tgg	gta	aga	gac	att	tat	ctg	ccg	cag	gga	ccc	698
81	Thr	Ala	Asn	Gly	Arg	Trp	Val	Arg	Asp	Ile	Tyr	Leu	Pro	Gln	Gly	Pro	
82			175					180						185			
84	gac	ctt	gaa	ggt	aag	atg	gtt	cgc	ttt	gtt	tcg	tct	gca	ggc	tat	agt	746
85	Asp	Leu	Glu	Gly	Lys	Met	Val	Arg	Phe	Val	Ser	Ser	Ala	Gly	Tyr	Ser	
86		190					195						200				
88	tca	acg	gtt	ttt	tat	ggt	gat	cga	aaa	gtc	aca	ctc	tcg	gtg	ggt	aac	794
89	Ser	Thr	Val	Phe	Tyr	Gly	Asp	Arg	Lys	Val	Thr	Leu	Ser	Val	Gly	Asn	
90		205				210					215						
92	act	ctt	ctg	ttc	aaa	tat	gta	aat	ggt	cag	tgg	ttc	cgc	tcc	ggt	gaa	842
93	Thr	Leu	Leu	Phe	Lys	Tyr	Val	Asn	Gly	Gln	Trp	Phe	Arg	Ser	Gly	Glu	
94	220				225					230					235		
96	ctg	gag	aat	aat	cga	atc	act	tat	gct	cag	cat	att	tgg	agt	gct	gaa	890
97	Leu	Glu	Asn	Asn	Arg	Ile	Thr	Tyr	Ala	Gln	His	Ile	Trp	Ser	Ala	Glu	
98			240						245					250			
100	ctg	cct	gcg	cac	tgg	atc	gtg	cct	ggt	tta	aac	ttg	gtg	att	aaa	cag	938
101	Leu	Pro	Ala	His	Trp	Ile	Val	Pro	Gly	Leu	Asn	Leu	Val	Ile	Lys	Gln	
102			255					260						265			
104	ggc	aat	ctg	agc	ggt	cgc	cta	aat	gat	atc	aag	att	gga	gca	ccg	ggt	986
105	Gly	Asn	Leu	Ser	Gly	Arg	Leu	Asn	Asp	Ile	Lys	Ile	Gly	Ala	Pro	Gly	
106		270					275						280				
108	gag	ctg	ttg	ttg	cat	aca	att	gat	atc	ggg	atg	ttg	acc	act	ccc	cgg	1034
109	Glu	Leu	Leu	Leu	His	Thr	Ile	Asp	Ile	Gly	Met	Leu	Thr	Thr	Pro	Arg	
110		285				290						295					
112	gat	cgc	ttt	gat	ttt	gcc	aaa	gac	aaa	gaa	gca	cat	agg	gaa	tat	ttc	1082
113	Asp	Arg	Phe	Asp	Phe	Ala	Lys	Asp	Lys	Glu	Ala	His	Arg	Glu	Tyr	Phe	
114	300				305					310					315		
116	cag	acc	att	cct	gta	agt	cgt	atg	att	gtt	aat	aat	tat	gcg	cct	cta	1130
117	Gln	Thr	Ile	Pro	Val	Ser	Arg	Met	Ile	Val	Asn	Asn	Tyr	Ala	Pro	Leu	
118			320					325					330				
120	cac	cta	aag	gaa	gtt	atg	tta	cca	acc	gga	gag	tta	ttg	aca	gat	atg	1178
121	His	Leu	Lys	Glu	Val	Met	Leu	Pro	Thr	Gly	Glu	Leu	Leu	Thr	Asp	Met	
122			335					340					345				
124	gat	cca	gga	aat	ggt	ggg	tgg	cat	agt	ggt	aca	atg	cgt	caa	aga	ata	1226
125	Asp	Pro	Gly	Asn	Gly	Gly	Trp	His	Ser	Gly	Thr	Met	Arg	Gln	Arg	Ile	
126		350					355						360				
128	ggt	aaa	gaa	ttg	gtt	tcg	cat	ggc	att	gat	aat	gct	aac	tat	ggt	tta	1274
129	Gly	Lys	Glu	Leu	Val	Ser	His	Gly	Ile	Asp	Asn	Ala	Asn	Tyr	Gly	Leu	

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130	365	370	375	
132	aat agt acc gca ggc tta ggg gag aat agt cat cca tat gta gtt gcg	1322		
133	Asn Ser Thr Ala Gly Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala			
134	380 385 390 395			
136	caa tta gcg gca cat aat agc cgc ggt aat tat gct aat ggc atc cag	1370		
137	Gln Leu Ala Ala His Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln			
138	400 405 410			
140	gtt cat ggt ggc tcc gga ggt ggg gga att gtt act tta gat tcc aca	1418		
141	Val His Gly Gly Ser Gly Gly Gly Gly Ile Val Thr Leu Asp Ser Thr			
142	415 420 425			
144	ttg ggg aat gag ttc agt cat gaa gtt ggt cat aat tat ggt ctt ggt	1466		
145	Leu Gly Asn Glu Phe Ser His Glu Val Gly His Asn Tyr Gly Leu Gly			
146	430 435 440			
148	cat tat gta gat ggt ttc aag ggt tct gta cat cgt agt gca gaa aat	1514		
149	His Tyr Val Asp Gly Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn			
150	445 450 455			
152	aac aac tca act tgg gga tgg gat ggt gat aaa aaa cgg ttt att cct	1562		
153	Asn Asn Ser Thr Trp Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro			
154	460 465 470 475			
156	aac ttt tat ccg tct caa aca aat gaa aag agt tgt ctg aat aat cag	1610		
157	Asn Phe Tyr Pro Ser Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln			
158	480 485 490			
160	tgt caa gaa ccg ttt gat gga cac aaa ttt ggt ttt gac gcc atg gcg	1658		
161	Cys Gln Glu Pro Phe Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala			
162	495 500 505			
164	gga ggc agc cct ttc tct gct gca aac cgt ttc aca atg tat act ccg	1706		
165	Gly Gly Ser Pro Phe Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro			
166	510 515 520			
168	aat tca tcg gct atc atc cag cgt ttt ttt gaa aat aaa gct gtg ttc	1754		
169	Asn Ser Ser Ala Ile Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe			
170	525 530 535			
172	gat agc cgt tcc tcc acc ggc ttc agc aag tgg aat gca gat acg cag	1802		
173	Asp Ser Arg Ser Ser Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln			
174	540 545 550 555			
176	gaa atg gaa ccg tat gaa cac acc att gac cgt gcg gag cag att acg	1850		
177	Glu Met Glu Pro Tyr Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr			
178	560 565 570			
180	gct tca gtc aat gag cta agt gaa agc aaa atg gct gag ctg atg gca	1898		
181	Ala Ser Val Asn Glu Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala			
182	575 580 585			
184	gag tac gct gtc gtc aaa gtg cat atg tgg aac ggt aac tgg aca aga	1946		
185	Glu Tyr Ala Val Val Lys Val His Met Trp Asn Gly Asn Trp Thr Arg			
186	590 595 600			
188	aac atc tat atc cct aca gcc tcc gca gat aat aga ggc agt atc ctg	1994		
189	Asn Ile Tyr Ile Pro Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu			
190	605 610 615			
192	acc atc aac cat gag gcc ggt tat aat agt tat ctg ttt ata aat ggt	2042		
193	Thr Ile Asn His Glu Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly			
194	620 625 630 635			

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196 gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc ttt gtt tcc gat 2090
197 Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp
198 640 645 650
200 ggt cag ttc tgg aaa gaa cgt gat gtg gtt gat act cgt gaa gcg cgt 2138
201 Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg
202 655 660 665
204 aag cca gag cag ttt ggt gtt cct gtg acg acc ctg gtg ggg tat tac 2186
205 Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr
206 670 675 680
208 gat ccg gaa ggc acg ctg tca agc tac atc tat cct gcg atg tat ggt 2234
209 Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly
210 685 690 695
212 gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac 2282
213 Ala Tyr Gly Phe Thr Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn
214 700 705 710 715
216 gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga 2330
217 Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg
218 720 725 730
220 ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att 2378
221 Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile
222 735 740 745
224 aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat 2426
225 Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn
226 750 755 760
228 aac aag ata ctg gat acc aaa tcg ctc aca cct gcg cca gaa gga ctt 2474
229 Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu
230 765 770 775
232 acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga 2522
233 Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly
234 780 785 790 795
236 tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt 2570
237 Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly
238 800 805 810
240 caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc 2618
241 Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val
242 815 820 825
244 tat gtc gac agc ggg gct aaa gcg aaa gtg ctg ctt tct gac tgg gat 2666
245 Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp
246 830 835 840
248 aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca 2714
249 Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro
250 845 850 855
252 gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc 2762
253 Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe
254 860 865 870 875
256 agt aaa cct agg tca atg agg gtt gta tat aaa taa 2798
257 Ser Lys Pro Arg Ser Met Arg Val Val Tyr Lys
258 880 885
261 <210> SEQ ID NO: 2

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Input Set : A:\B0122173.txt

Output Set: N:\CRF3\02262002\J002309A.raw

262 <211> LENGTH: 886  
 263 <212> TYPE: PRT  
 264 <213> ORGANISM: Unknown Organism  
 W--> 266 <220> FEATURE:  
 W--> 266 <223> OTHER INFORMATION:  
 266 <400> SEQUENCE: 2

*see error summary sheet,  
item 11*

268 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu Ala Pro Leu Ala Ile  
 269 1 5 10 15  
 272 Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn Ser Ala Ile Tyr Phe  
 273 20 25 30  
 276 Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu  
 277 35 40 45  
 280 Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly  
 281 50 55 60  
 284 Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val  
 285 65 70 75 80  
 288 Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg  
 289 85 90 95  
 292 Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser  
 293 100 105 110  
 296 Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly  
 297 115 120 125  
 300 Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val  
 301 130 135 140  
 304 Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
 305 145 150 155 160  
 308 His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg  
 309 165 170 175  
 312 Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys  
 313 180 185 190  
 316 Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr  
 317 195 200 205  
 320 Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys  
 321 210 215 220  
 324 Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg  
 325 225 230 235 240  
 328 Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp  
 329 245 250 255  
 332 Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly  
 333 260 265 270  
 336 Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His  
 337 275 280 285  
 340 Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe  
 341 290 295 300  
 344 Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe Gln Thr Ile Pro Val  
 345 305 310 315 320  
 348 Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu His Leu Lys Glu Val  
 349 325 330 335  
 352 Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met Asp Pro Gly Asn Gly



VERIFICATION SUMMARY

DATE: 02/26/2002

PATENT APPLICATION: US/10/002,309A

TIME: 14:53:41

Input Set : A:\B0122173.txt

Output Set: N:\CRF3\02262002\J002309A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:266 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:266 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: